

SEQUENCE LISTING

<110> Lee, Arthur M.E.
Jain, Mukesh
Watanabe, Masafumi

<120> IN VITRO DIFFERENTIATION OF VASCULAR SMOOTH MUSCLE
CELLS AND REAGENTS RELATED THERETO

<130> APV-382.01

<140> 09/181,311

<141> 1998-10-28

<150> 60/063,363

<151> 1997-10-28

<150> 60/080,420

<151> 1998-04-02

<150> 60/096,685

<151> 1998-08-14

<160> 23

<170> PatentIn Ver. 2.0

<210> 1

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<212> DNA

<213> Murine

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<223> Clone WO11

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gattcagggtg tggatcgtca gcctaggcga aga 153

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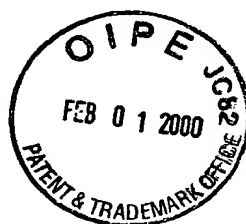
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<213> Homo sapiens



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 35 40 45
 Pro Arg Glu Asp Asp Val Glu Ala Pro Pro Pro Pro Glu Pro Thr Pro
 50 55 60
 Arg Val Arg Lys Ala Gln Ala Gly Gly Lys Pro Gly Pro Gly Thr Ala
 65 70 75 80
 Ala Glu Val Pro Pro Glu Lys Thr Lys Asp Lys Gly Lys Lys Gly Lys
 85 90 95
 Lys Asp Lys Gly Pro Lys Val Pro Lys Glu Ser Leu Glu Gly Ser Pro
 100 105 110
 Arg Pro Pro Lys Lys Gly Lys Glu Lys Pro Pro Lys Ala Thr Lys Lys
 115 120 125
 Pro Lys Glu Lys Pro Pro Lys Ala Thr Lys Lys Pro Lys Glu Glu Pro
 130 135 140
 Pro Lys Ala Thr Lys Lys Pro Lys Glu Lys Lys Ala Thr Lys Lys Pro
 145 150 155 160
 Pro Ser Gly Lys Arg Pro Pro Ile Leu Ala Pro Ser Glu Thr Leu Glu
 165 170 175
 Trp Pro Leu Pro Pro Pro Pro Ser Pro Gly Pro Glu Glu Leu Pro Gln
 180 185 190
 Glu Gly Gly Ala Pro Leu Ser Asn Asn Trp Gln Asn Pro Gly Glu Glu
 195 200 205
 Thr His Val Glu Ala Gln Glu His Gln Pro Glu Pro Glu Glu Glu Thr
 210 215 220
 Glu Gln Pro Thr Leu Asp Tyr Asn Ile Glu Arg Glu Asp Tyr Glu Asp
 225 230 235 240
 Phe Glu Tyr Ile Arg Arg Gln Lys Gln Pro Arg Pro Pro Pro Ser Arg
 245 250 255
 Arg Arg Arg Pro Glu Arg Val Trp Pro Glu Pro Pro Glu Glu Lys Ala
 260 265 270
 Pro Ala Pro Ala Pro Glu Glu Arg Ile Glu Pro Pro Val Lys Pro Leu
 275 280 285

Leu Pro Pro Leu Pro Pro Asp Tyr Gly Asp Gly Tyr Val Ile Pro Asn
 290 295 300
 Tyr Asp Asp Met Asp Tyr Gly Pro Pro Pro Pro Gln Lys Pro Asp Ala
 305 310 315 320
 Glu Arg Gln Thr Asp Glu Glu Lys Glu Glu Leu Lys Lys Pro Lys Lys
 325 330 335
 Glu Asp Ser Ser Pro Lys Glu Glu Thr Asp Lys Trp Ala Val Glu Lys
 340 345 350
 Gly Lys Asp His Lys Glu Pro Arg Lys Gly Glu Glu Leu Glu Glu Glu
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 Trp Thr Pro Thr Glu Lys Val Lys Cys Pro Pro Ile Gly Met Glu Ser
 370 375 380
 His Arg Ile Asn Gln Ile Arg Ala Ser Ser Met Leu Arg His Gly Leu
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 Gly Ala Gln Arg Gly Arg Leu Asn Met Gln Thr Gly Ala Thr Glu Asp
 405 410 415
 Asp Tyr Tyr Asp Gly Ala Trp Cys Ala Glu Asp Asp Ala Arg Thr Gln
 420 425 430
 Trp Ile Glu Val Asp Thr Arg Arg Thr Thr Arg Phe Thr Gly Val Ile
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 Thr Gln Gly Arg Asp Ser Ser Ile His Asp Asp Phe Val Thr Thr Phe
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 465 470 475 480
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 515 520 525
 Ser Val Ala Pro Val Tyr Ser Tyr Tyr Ala Gln Asn Glu Val Val Asp
 530 535 540
 Asp Leu Asp Phe Arg His His Ser Tyr Lys Asp Met Arg Gln Leu Met
 545 550 555 560
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 565 570 575
 Gly Lys Ser Ser Arg Gly Leu Lys Ile Tyr Ala Met Glu Ile Ser Asp
 580 585 590

Asn Pro Gly Glu His Glu Leu Gly Glu Pro Glu Phe Arg Tyr Thr Ala
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 Gly Ile His Gly Asn Glu Val Leu Gly Arg Glu Leu Ile Leu Met Gln
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 Tyr Leu Cys Arg Glu Tyr Arg Asp Gly Asn Pro Arg Val Arg Ser Leu
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 675 680 685
 Leu Asn Ser Val Leu Trp Gly Ala Glu Glu Phe Val Pro Tyr Arg Val
 690 695 700
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 Thr Val Ser Thr Glu Val Arg Ala Ile Ile Ala Trp Met Glu Lys Asn
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 Pro Phe Val Leu Gly Ala Asn Leu Asn Gly Gly Glu Arg Leu Val Ser
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 Ala Ala Met Ala Ala Ala Glu Gly Glu Asp Glu Val Ser Glu Ala Gln
 770 775 780
 Glu Thr Pro Asp His Ala Ile Phe Arg Trp Leu Ala Ile Ser Phe Ala
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 Ser Ala His Leu Thr Leu Thr Glu Pro Tyr Arg Gly Gly Cys Gln Ala
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 820 825 830
 Pro Arg Thr Gly Thr Ile Asn Asp Phe Ser Tyr Leu His Thr Asn Cys
 835 840 845
 Leu Glu Leu Ser Phe Tyr Ile Asp Lys Phe Pro His Glu Ser Glu Leu
 850 855 860
 Pro Arg Glu Trp Glu Asn Asn Lys Glu Ala Leu Leu Thr Phe Met Glu
 865 870 875 880
 Gln Val His Arg Gly Ile Lys Gly Val Val Thr Asp Glu Gln Gly Ile
 885 890 895

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Lys Thr Ala Ser Gly Gly Asp Tyr Trp Arg Ile Leu Asn Pro Gly Glu
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Tyr Arg Val Thr Ala Glu Gly Tyr Thr Pro Ser Ala Lys Thr Cys Asn
930 935 940

Val Asp Tyr Asp Ile Gly Ala Thr Gln Cys Asn Phe Ile Leu Ala Arg
945 950 955 960

Ser Asn Trp Lys Arg Ile Arg Glu Ile Met Ala Met Asn Gly Asn Arg
965 970 975

Pro Ile Pro His Ile Asp Pro Ser Arg Pro Met Thr Pro Gln Gln Arg
980 985 990

Arg Leu Gln Gln Arg Arg Leu Gln His Arg Leu Arg Leu Arg Ala Gln
995 1000 1005

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Trp Gly Leu Ile Pro Pro Thr Thr Ala Gly Trp Glu Glu Ser Glu Thr
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Glu Thr Tyr Thr Glu Val Val Thr Glu Phe Gly Thr Glu Val Glu Pro
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Glu Phe Gly Thr Lys Val Glu Pro Glu Phe Glu Thr Gln Leu Phe Glu
1075 1080 1085

Thr Gln Leu Glu Pro Glu Phe Glu Glu Glu Glu Glu Glu Lys Glu
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Tyr Thr Val Asn Phe Gly Asp Phe
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 35 40 45
 Ser Pro Pro Arg Glu Asp Asp Val Glu Val Gln Pro Leu Pro Glu Pro
 50 55 60
 Thr Gln Arg Pro Arg Lys Ser Lys Ala Gly Gly Lys Gln Arg Ala Asp
 65 70 75 80
 Val Glu Val Pro Pro Glu Lys Asn Lys Asp Lys Glu Lys Lys Gly Lys
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 Lys Asp Lys Gly Pro Lys Ala Thr Lys Pro Leu Glu Gly Ser Thr Arg
 100 105 110
 Pro Thr Lys Lys Pro Lys Glu Lys Pro Pro Lys Ala Thr Lys Lys Pro
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 Ala Gly Lys Lys Phe Ser Thr Val Ala Pro Leu Glu Thr Leu Asp Arg
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 Arg Asp Thr Pro Phe Pro Asn Ala Trp Gln Gly Gln Gly Glu Glu Thr
 195 200 205
 Gln Val Glu Ala Lys Gln Pro Arg Pro Glu Pro Glu Glu Glu Thr Glu
 210 215 220
 Met Pro Thr Leu Asp Tyr Asn Ile Glu Lys Glu Asp Tyr Glu Asp Phe
 225 230 235 240
 Glu Tyr Ile Arg Arg Gln Lys Gln Pro Arg Pro Thr Pro Ser Arg Arg
 245 250 255
 Arg Leu Trp Pro Glu Arg Pro Glu Glu Lys Thr Glu Glu Pro Glu Glu
 260 265 270
 Arg Lys Glu Val Glu Pro Pro Leu Lys Pro Leu Leu Pro Pro Asp Tyr
 275 280 285
 Gly Asp Ser Tyr Val Ile Pro Asn Tyr Asp Asp Leu Asp Tyr Pro His
 290 295 300
 Pro Pro Pro Gln Lys Pro Asp Val Gly Gln Glu Val Asp Glu Glu Lys
 305 310 315 320

Glu Glu Met Lys Lys Pro Lys Lys Glu Gly Ser Ser Pro Lys Glu Asp
 325 330 335
 Thr Glu Asp Lys Trp Thr Val Glu Lys Asn Lys Asp His Lys Gly Pro
 340 345 350
 Arg Lys Gly Glu Glu Leu Glu Glu Trp Ala Pro Val Glu Lys Ile
 355 360 365
 Lys Cys Pro Pro Ile Gly Met Glu Ser His Arg Ile Asn Gln Ile Arg
 370 375 380
 Ala Ser Ser Met Leu Arg His Gly Leu Gly Ala Gln Arg Gly Arg Leu
 385 390 395 400
 Asn Met Gln Ala Gly Ala Asn Glu Asp Asp Tyr Tyr Asp Gly Ala Trp
 405 410 415
 Cys Ala Glu Asp Glu Ser Gln Thr Gln Trp Ile Glu Val Asp Thr Arg
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 Arg Thr Thr Arg Phe Thr Gly Val Ile Thr Gln Gly Arg Asp Ser Ser
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 Ile His Asp Asp Phe Val Thr Thr Phe Phe Phe Ser Asn Asp Ser Gln
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 Thr Trp Val Met Tyr Thr Asn Gly Tyr Glu Glu Met Thr Phe Tyr Gly
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 485 490 495
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 Cys Met Arg Leu Glu Val Leu Gly Cys Pro Val Thr Pro Val Tyr Ser
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 Ser Tyr Lys Asp Met Arg Gln Leu Met Lys Ala Val Asn Glu Glu Cys
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 Pro Thr Ile Thr Arg Thr Tyr Ser Leu Gly Lys Ser Ser Arg Gly Leu
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 Lys Ile Tyr Ala Met Glu Ile Ser Asp Asn Pro Gly Asp His Glu Leu
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 Gly Glu Pro Glu Phe Arg Tyr Thr Ala Gly Ile His Gly Asn Glu Val
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 Leu Gly Arg Glu Leu Ile Leu Met Gln Tyr Leu Cys Gln Glu Tyr Arg
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Asp Gly Asn Pro Arg Val Arg Asn Leu Val Gln Asp Thr Arg Ile His
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 Leu Val Pro Ser Leu Asn Pro Asp Gly Tyr Glu Val Ala Ala Gln Met
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 Gly Ser Glu Phe Gly Asn Trp Ala Leu Gly Leu Trp Thr Glu Glu Gly
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 Phe Asp Ile Phe Glu Asp Phe Pro Asp Leu Asn Ser Val Leu Trp Ala
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 Gly Glu Asp Gly Val Ser Glu Ala Gln Glu Thr Pro Asp His Ala Ile
 770 775 780
 Phe Arg Trp Leu Ala Ile Ser Phe Ala Ser Ala His Leu Thr Met Thr
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 Glu Pro Tyr Arg Gly Gly Cys Gln Ala Gln Asp Tyr Thr Ser Gly Met
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 Gly Ile Val Asn Gly Ala Lys Trp Asn Pro Arg Ser Gly Thr Phe Asn
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 Asp Phe Ser Tyr Leu His Thr Asn Cys Leu Glu Leu Ser Val Tyr Ile
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 Asp Lys Phe Pro His Glu Ser Glu Leu Pro Arg Glu Trp Glu Asn Asn
 850 855 860
 Lys Glu Ala Leu Leu Thr Phe Met Glu Gln Val His Arg Gly Ile Lys
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 Gly Val Val Thr Asp Glu Gln Gly Ile Pro Ile Ala Asn Ala Thr Ile
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 Ser Val Ser Gly Ile Asn His Gly Val Lys Thr Ala Ser Gly Gly Asp
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 Tyr Trp Arg Ile Leu Asn Pro Gly Glu Tyr Arg Val Thr Ala Glu Gly
 915 920 925

Tyr Thr Ser Ser Ala Lys Ile Cys Asn Val Asp Tyr Asp Ile Gly Ala
 930 935 940
 Thr Gln Cys Asn Phe Ile Leu Ala Arg Ser Asn Trp Lys Arg Ile Arg
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 995 1000 1005
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<220>
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<400> 5
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10

<210> 6
 <211> 30
 <212> DNA
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30

<210> 7
 <211> 10

<212> DNA
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<220>
 <223> Description of Artificial Sequence: modified oligo

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<210> 8
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<400> 8
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<212> DNA

<213> Artificial Sequence

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<211> 21

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 <223> Description of Artificial Sequence: EcoRI site

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<223> Description of Artificial Sequence: HindIII site

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28

